

# NCBI Conserved Domain Search

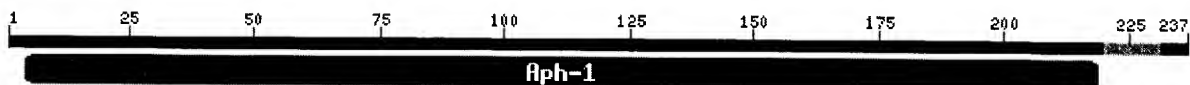
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[CDD](#)
[Taxonomy](#)
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RPS-BLAST 2.2.9 [May-01-2004]

Query= local sequence:  
(237 letters)

Database: cdd.v2.00  
11,382 PSSMs; 2,824,437 total columns

Click on boxes for multiple alignments



Show Domain Relatives

PSSMs producing significant alignments: Score E  
(bits) value

[gnl|CDD|26475](#) pfam06105, Aph-1, Aph-1 protein. This family consists of sever... [191](#) 6e-50

[gnl|CDD|26475](#), pfam06105, Aph-1, Aph-1 protein. This family consists of several eukaryotic Aph-1 proteins. Gamma-secretase catalyses the intramembrane proteolysis of Notch, beta-amyloid precursor protein, and other substrates as part of a new signaling paradigm and as a key step in the pathogenesis of Alzheimer's disease. It is thought that the presenilin heterodimer comprises the catalytic site and that a highly glycosylated form of nicastrin associates with it. Aph-1 and Pen-2, two membrane proteins genetically linked to gamma-secretase, associate directly with presenilin and nicastrin in the active protease complex. Co-expression of all four proteins leads to marked increases in presenilin heterodimers, full glycosylation of nicastrin, and enhanced gamma-secretase activity.

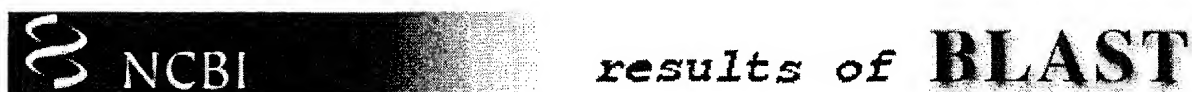
CD-Length = 246 residues, 95.1% aligned  
Score = 191 bits (487), Expect = 6e-50

|        |     |  |     |
|--------|-----|--|-----|
| Query: | 4   | VFFGCAFIAGFP--MMYVFTIAEEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD   | 59  |
| Sbjct: | 5   | VFFGCTFIAFGPSLALFVSTIARDPLRIIILIAGAFFWLVSLLLSSLVWFILVPLTDKAD   | 64  |
| Query: | 60  | GPTQKYLILFGAWSWI--QEMF--AAYKLLK-MSEGLKSINPGETAPSMRLM--YVSGLG   | 112 |
| Sbjct: | 65  | AWWQYGLLIFGVVSVCFQELFRFAYYKLLKKAEEGLDSIAEDGRRPISKRLAYVSGLG     | 124 |
| Query: | 113 | FGIMSGVFSM--TLDSDLGPGTVGIHGDSPPQFFLYSA-GTLVIILLHVFVGIVFFDGCCEM | 169 |
| Sbjct: | 125 | FGIISGVFSVNNILADALGPGTVGIHGDSKLEFLTSAFMALAIILLHTFWGVVFFDACEK   | 184 |
| Query: | 170 | --KWGILLIALTHLLVSAQTFISSYYGINLM-AFIILVV-GTWAFIAAGGSCRS         | 219 |
| Sbjct: | 185 | NNYIALGIVPVSHLLVSMLTFLNPAYEGSLVPLYLVLSLMGVWAFVAGGSLRS          | 238 |

**Citing CD-Search:** Marchler-Bauer A, Anderson JB, DeWeese-Scott C, Fedorova ND, Geer LY, He S,

Hurwitz DI, Jackson JD, Jacobs AR, Lanczycki CJ, Liebert CA, Liu C, Madej T, Marchler GH, Mazumder R, Nikolskaya AN, Panchenko AR, Rao BS, Shoemaker BA, Simonyan V, Song JS, Thiessen PA, Vasudevan S, Wang Y, Yamashita RA, Yin JJ, and Bryant SH (2003), "*CDD: a curated Entrez database of conserved domain alignments*", **Nucleic Acids Res.** **31**:383-387.

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**BLASTP 2.2.9 [May-01-2004]**Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1087209714-1737-5403932422.BLASTQ4

**Query=**

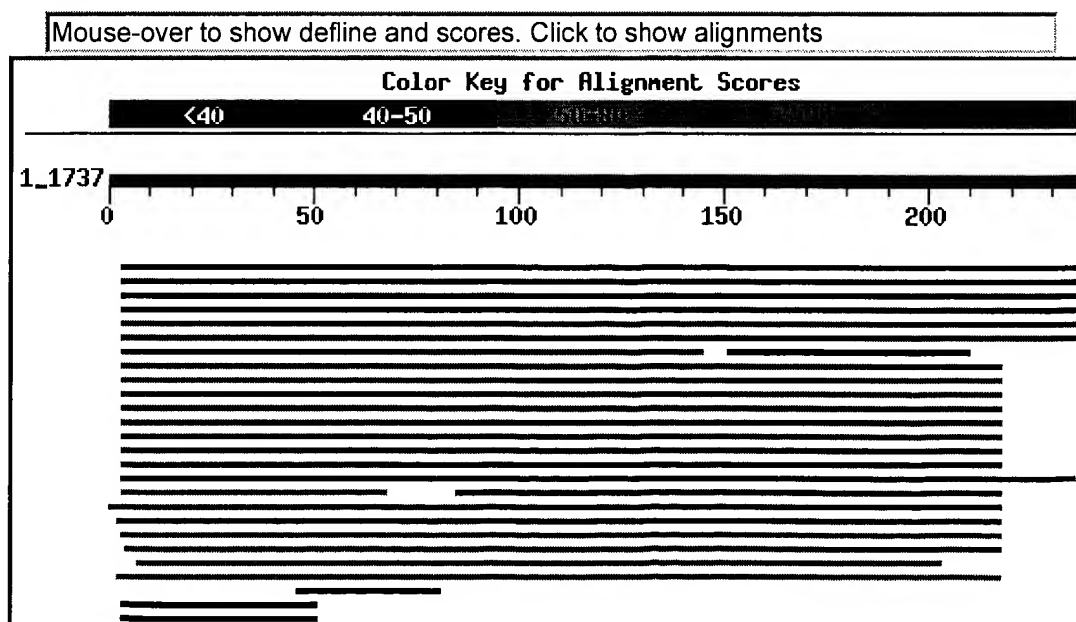
(237 letters)

**Database:** All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF excluding environmental samples  
1,860,402 sequences; 617,572,895 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

**Distribution of 28 Blast Hits on the Query Sequence**

Sequences producing significant alignments:

Score E  
(bits) Value

|  |   |                     |                       |                   |
|--|---|---------------------|-----------------------|-------------------|
| <a href="#">gi 18088649 gb AAH20905.1 </a>       | Presenilin stabilization factor-...           | <a href="#">283</a> | <a href="#">3e-75</a> | <a href="#">L</a> |
| <a href="#">gi 13775224 ref NP_112591.1 </a>     | presenilin stabilization facto...             | <a href="#">281</a> | <a href="#">8e-75</a> | <a href="#">L</a> |
| <a href="#">gi 37182518 gb AAQ89061.1 </a>       | TAAV688 [Homo sapiens]                        | <a href="#">281</a> | <a href="#">8e-75</a> |                   |
| <a href="#">gi 29243936 ref NP_808251.1 </a>     | hypothetical protein 4632417K0...             | <a href="#">247</a> | <a href="#">2e-64</a> | <a href="#">L</a> |
| <a href="#">gi 34864291 ref XP_217185.2 </a>     | similar to RIKEN cDNA 0610008A...             | <a href="#">240</a> | <a href="#">2e-62</a> | <a href="#">L</a> |
| <a href="#">gi 21492616 ref NP_080950.1 </a>     | RIKEN cDNA 0610008A10 [Mus mus...             | <a href="#">233</a> | <a href="#">2e-60</a> | <a href="#">L</a> |
| <a href="#">gi 26324468 dbj BAC25988.1 </a>      | unnamed protein product [Mus mu...            | <a href="#">186</a> | <a href="#">5e-46</a> | <a href="#">L</a> |
| <a href="#">gi 37077149 sp Q8BVF7 AP1A MOUSE</a> | Gamma-secretase subunit AP...                 | <a href="#">176</a> | <a href="#">2e-43</a> | <a href="#">L</a> |
| <a href="#">gi 12654775 gb AAH01230.1 </a>       | APH-1A protein [Homo sapiens]                 | <a href="#">176</a> | <a href="#">3e-43</a> | <a href="#">L</a> |
| <a href="#">gi 37077707 sp Q96BI3 AP1A HUMAN</a> | Gamma-secretase subunit AP...                 | <a href="#">176</a> | <a href="#">3e-43</a> | <a href="#">L</a> |
| <a href="#">gi 34858248 ref XP_345252.1 </a>     | similar to Aphla-pending prote...             | <a href="#">176</a> | <a href="#">3e-43</a> | <a href="#">L</a> |
| <a href="#">gi 7705787 ref NP_057106.1 </a>      | CGI-78 protein [Homo sapiens] >...            | <a href="#">173</a> | <a href="#">3e-42</a> | <a href="#">L</a> |
| <a href="#">gi 22203751 ref NP_666216.1 </a>     | anterior pharynx defective 1A ...             | <a href="#">172</a> | <a href="#">5e-42</a> | <a href="#">L</a> |
| <a href="#">gi 14250557 gb AAH08732.1 </a>       | APH-1A protein [Homo sapiens] >g...           | <a href="#">172</a> | <a href="#">6e-42</a> | <a href="#">L</a> |
| <a href="#">gi 41056229 ref NP_956409.1 </a>     | anterior pharynx defective 1B ...             | <a href="#">171</a> | <a href="#">1e-41</a> | <a href="#">L</a> |
| <a href="#">gi 34864287 ref XP_343418.1 </a>     | similar to RIKEN cDNA 0610008A...             | <a href="#">171</a> | <a href="#">1e-41</a> | <a href="#">L</a> |
| <a href="#">gi 26347159 dbj BAC37228.1 </a>      | unnamed protein product [Mus mu...            | <a href="#">120</a> | <a href="#">2e-26</a> | <a href="#">L</a> |
| <a href="#">gi 31233667 ref XP_318923.1 </a>     | ENSANGP00000015809 [Anopheles ...             | <a href="#">117</a> | <a href="#">2e-25</a> |                   |
| <a href="#">gi 47214485 emb CAG12490.1 </a>      | unnamed protein product [Tetrao...            | <a href="#">116</a> | <a href="#">4e-25</a> |                   |
| <a href="#">gi 48095709 ref XP_392345.1 </a>     | similar to CG2855-PA [Apis mel...             | <a href="#">116</a> | <a href="#">5e-25</a> | <a href="#">L</a> |
| <a href="#">gi 20129183 ref NP_608710.1 </a>     | CG2855-PA [Drosophila melanoga...             | <a href="#">105</a> | <a href="#">1e-21</a> | <a href="#">L</a> |
| <a href="#">gi 39580694 emb CAE70374.1 </a>      | Hypothetical protein CBG16933 [...            | <a href="#">64</a>  | <a href="#">2e-09</a> |                   |
| <a href="#">gi 20829201 ref XP_129583.1 </a>     | similar to CGI-78 protein [Mus...             | <a href="#">57</a>  | <a href="#">4e-07</a> |                   |
| <a href="#">gi 17509423 ref NP_492469.1 </a>     | i-78 protein like, Anterior PH...             | <a href="#">52</a>  | <a href="#">1e-05</a> | <a href="#">L</a> |
| <a href="#">gi 48129682 ref XP_393309.1 </a>     | similar to Na/Ca exchange prot...             | <a href="#">33</a>  | <a href="#">5.3</a>   | <a href="#">L</a> |
| <a href="#">gi 48103053 ref XP_395490.1 </a>     | similar to CG5880-PA [Apis mel...             | <a href="#">32</a>  | <a href="#">7.6</a>   | <a href="#">L</a> |
| <a href="#">gi 16763476 ref NP_459091.1 </a>     | glutathione-regulated K <sup>+</sup> efflu... | <a href="#">32</a>  | <a href="#">9.6</a>   |                   |
| <a href="#">gi 16759081 ref NP_454698.1 </a>     | glutathione-regulated potassiu...             | <a href="#">32</a>  | <a href="#">9.6</a>   |                   |

## Alignments

Get selected sequences

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Deselect all

☐ >[gi|18088649|gb|AAH20905.1|](#) [L](#) Presenilin stabilization factor-like [Homo sapiens]  
Length = 257

Score = 283 bits (723), Expect = 3e-75

Identities = 202/253 (79%), Positives = 211/253 (83%), Gaps = 19/253 (7%)

Query: 4 VFFGCAFIAGPMM--YVFTIAEEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59

VFFGCAFIAGFP + YVFTIA EPLRIIFLIAGAF LVSLLISSL WFMARV IDNKD

Sbjct: 5 VFFGCAFIAGFPALALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKD 64

Query: 60 GPTQKYLILFGAWS--WIQEMF--AYYKLLK-MSEGLKSINPGETAPSMRLM-YVSGGLGF 113

GPTQKYLILFGA+ +IQEMF AYYKLLK SEGLKSINPGETAPSMRL+ YVSGGLGF

Sbjct: 65 GPTQKYLILFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGGLGF 124

Query: 114 GIMSGVFSM--TLSDSLGPGTVGIHGDSQPFFLYSA-GTLVIILLHVFWGIVFFDGCE-M 169

GIMSGVFS TLSDSLGPGTVGIHGDSQPFFLYSA TLVIILLHVFWGIVFFDGCE

Sbjct: 125 GIMSGVFSFVNTLSDSLGPSTVGIHGDSQPFFLYSAFMTLVIILLHVFWGIVFFDGCEK 184

Query: 170 KWG-ILLIALTHLLVSAQTFISSYYGINLM-AFIILVV-GTWAFIAAGGSCRS--XXXXX 224  
 KWG +L++ LTHLLVSAQTFISSYYGINL AFIILV+ GTWAF+AAGGSCRS  
 Sbjct: 185 KWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSCLKCLLC 244

Query: 225 XXXXXXXXYNQRSR 237  
 YNQRSR  
 Sbjct: 245 QDKNFLLYNQRSR 257

☐ >gi|13775224|ref|NP\_112591.1| ☒ presenilin stabilization factor-like [Homo sapie  
 gi|37077447|sp|Q8WW43|AP1B\_HUMAN ☒ Gamma-secretase subunit APH-1B (APH-1b) (Aph-1  
 stabilization factor-like)  
 gi|12052866|emb|CAB66606.1| ☒ hypothetical protein [Homo sapiens]  
 gi|24637564|gb|AAN63817.1| ☒ presenilin stabilization factor-like protein [Homo s  
 Length = 257

Score = 281 bits (719), Expect = 8e-75  
 Identities = 201/253 (79%), Positives = 211/253 (83%), Gaps = 19/253 (7%)

Query: 4 VFFGCAFIAGPMM--YVFTIAEEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGCAFIAGFP + YVFTIA EPLRIIFLIAGAF LVSLLISSL WFMARV IDNKD  
 Sbjct: 5 VFFGCAFIAGFPALALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKD 64

Query: 60 GPTQKYLIFGAWS--WIQEMF--AAYKLLK-MSEGLKSINPGETAPSMRLM-YVSGGLGF 113  
 GPTQKYLIFGA+ +I+EMF AAYKLLK SEGLKSINPGETAPSMRL+ YVSGGLGF  
 Sbjct: 65 GPTQKYLIFGAFVSVYIREMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGGLGF 124

Query: 114 GIMSGVFSM--TLSDSLGPGTVGIHGDSPOFFLYSA-GTLVIILLHVFWGIVFFDGCE-M 169  
 GIMSGVFS TLSDSLGPGTVGIHGDSPOFFLYSA TLVIILLHVFWGIVFFDGCE  
 Sbjct: 125 GIMSGVFSFVNTLSDSLGPSTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDGCEKK 184

Query: 170 KWG-ILLIALTHLLVSAQTFISSYYGINLM-AFIILVV-GTWAFIAAGGSCRS--XXXXX 224  
 KWG +L++ LTHLLVSAQTFISSYYGINL AFIILV+ GTWAF+AAGGSCRS  
 Sbjct: 185 KWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSCLKCLLC 244

Query: 225 XXXXXXXXYNQRSR 237  
 YNQRSR  
 Sbjct: 245 QDKNFLLYNQRSR 257

☐ >gi|37182518|gb|AAQ89061.1| TAAV688 [Homo sapiens]  
 Length = 257

Score = 281 bits (719), Expect = 8e-75  
 Identities = 202/253 (79%), Positives = 211/253 (83%), Gaps = 19/253 (7%)

Query: 4 VFFGCAFIAGPMM--YVFTIAEEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGCAFIAGFP + YVFTIA EPLRIIFLIAGAF LVSLLISSL WFMARV IDNKD  
 Sbjct: 5 VFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKD 64

Query: 60 GPTQKYLIFGAWS--WIQEMF--AAYKLLK-MSEGLKSINPGETAPSMRLM-YVSGGLGF 113  
 GPTQKYLIFGA+ +IQEMF AAYKLLK SEGLKSINPGETAPSMRL+ YVSGGLGF  
 Sbjct: 65 GPTQKYLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGGLGF 124

Query: 114 GIMSGVFSM--TLSDSLGPGTVGIHGDSPOFFLYSA-GTLVIILLHVFWGIVFFDGCE-M 169

GIMSGVFS TLSDSLGPGTVGIHGDSPQFFLYSA TLVIILLHVFWGIVFFDGCE  
 Sbjct: 125 GIMSGVFSFVNTLSDSLGPVTGVIHGDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKK 184

Query: 170 KWG-ILLIALTHLLVSAQTFISSYYGINLM-AFIILVV-GTWAFIAAGGSCRS--XXXXX 224  
 KWG +L++ LTHLLVSAQTFISSYYGINL AFIILV+ GTWAF+AAGGSCRS  
 Sbjct: 185 KWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSCLKCLLC 244

Query: 225 XXXXXXXYNQRSR 237  
 YNQRSR  
 Sbjct: 245 QDKNFLLYNQRSR 257

☐ >[gi|29243936|ref|NP\\_808251.1|](#) ☒ hypothetical protein 4632417K02 [Mus musculus]  
[gi|37077156|sp|Q8C7N7|AP1B\\_MOUSE](#) Gamma-secretase subunit APH-1B  
[gi|26340556|dbj|BAC33940.1|](#) ☒ unnamed protein product [Mus musculus]  
 Length = 257

Score = 247 bits (630), Expect = 2e-64  
 Identities = 173/253 (68%), Positives = 195/253 (77%), Gaps = 19/253 (7%)

Query: 4 VFFGCAFIAGPMM--YVFTIAEEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGCAFIAGFP + YVFTIA +PLR+IFLIAGAF LVSL+SS+ WF+ RV DN+D  
 Sbjct: 5 VFFGCAFIAGFPALALYVFTIATDPLRVIFLIAGAFFWLVSLLSSVFWFLVRVITDNRD 64

Query: 60 GPTQKYLLIFGAW--SWIQEMF--AYYKLLK-MSEGLKSINPGETAPSMRLM-YVSGLGF 113  
 GP Q YLLIFG IQE+F AYYKLLK SEGLKSINP ETAPSMRL+ YVSGLGF  
 Sbjct: 65 GPVQNYLLIFGVLLSVCIQELFRLAYYKLLKKASEGLKSINPEETAPSMRLLAYVSGLGF 124

Query: 114 GIMSGVFSM--TLSDSLGPGTVGIHGDSPQFFLYSA-GTLVIILLHVFWGIVFFDGCEM- 169  
 GIMSGVFS TLS+SLGPGTVGIHGDSPQFFL SA TLV+I+LHVFWG+VFFDGCE  
 Sbjct: 125 GIMSGVFSFVNTLSNSLGPVTGVIHGDSPQFFLNSAFMTLVVIMLHVFWGVVFFDGCEKN 184

Query: 170 KW-GILLIALTHLLVSAQTFISSYYGINLM-AFIILVV-GTWAFIAAGGSCRS--XXXXX 224  
 KW +L + LTHL+VS QTF+S YY +NL+ A+II+V+ G WAF AGGSCRS  
 Sbjct: 185 KWTLLTVLLTHLVVSTQTFSPYYEVLVTAYIIMVLMGIWAFYVAGGSCRSCLKCLLC 244

Query: 225 XXXXXXXYNQRSR 237  
 YNQRSR  
 Sbjct: 245 QDKDFLLYNQRSR 257

☐ >[gi|34864291|ref|XP\\_217185.2|](#) ☒ similar to RIKEN cDNA 0610008A10 [Rattus norvegi  
 Length = 257

Score = 240 bits (612), Expect = 2e-62  
 Identities = 171/253 (67%), Positives = 193/253 (76%), Gaps = 19/253 (7%)

Query: 4 VFFGCAFIAGPMM--YVFTIAEEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGCAFIAGFP + Y+FTIA +PLR+IFLIAGAF LVSL+SS+ WF+ RV DN+D  
 Sbjct: 5 VFFGCAFIAGFPALALYLFTIATDPLRVIFLIAGAFFWLVSLLSSVFWFLVRVITDNRD 64

Query: 60 GPTQKYLLIFGAW--SWIQEMF--AYYKLLK-MSEGLKSINPGETAPSMRLM-YVSGLGF 113  
 GP Q YLLIFG IQE+F AYY+LLK SEGLKSINP ETAPSMRL+ YVSGLGF  
 Sbjct: 65 GPVQNYLLIFGVLLSVCIQELFRLAYYRLLKKASEGLKSINPEETAPSMRLLAYVSGLGF 124

Query: 114 GIMSGVFSM--TLSDSLGPGTVGIHGDSPQFFLYSA-GTLVIILLHVFWGIVFFDGCEM- 169  
 GIMSGVFS TLS++LGPVTGVIHGDSPQFFL SA TLVII+LHVFWGIVFFDGCE

Sbjct: 125 GIMSGVFSFVNTLSNALGPGTVGIHGDSPPQFFLNSAFMTLVIIMLHVFWGIVFFDGCEKN 184

Query: 170 KWGI-LLIALTHLLVSAQTFISSYYGINLM-AFIILVV-GTWAFIAAGGSCRS--XXXXX 224  
 KW I L + LTHLLVS QT +S +Y +NL+ A+II+V+ G WAF AGGS RS

Sbjct: 185 KWIYILLTVLLTHLLVSTQTLLSPHYEVNLVTAYIIMVLMGIWAFVAGGSRRSLKCLLC 244

Query: 225 XXXXXXXXYNQRSR 237  
 YNQRSR

Sbjct: 245 QDKDFLLYNQRSR 257

☐ >gi|21492616|ref|NP\_080950.1| ☒ RIKEN cDNA 0610008A10 [Mus musculus]  
 gi|37077773|sp|Q9DCZ9|AP1C\_MOUSE ☒ Putative gamma-secretase subunit APH-1C  
 gi|12832198|dbj|BAB22004.1| ☒ unnamed protein product [Mus musculus]  
 gi|29747906|gb|AAH50923.1| ☒ RIKEN cDNA 0610008A10 [Mus musculus]  
 gi|38648719|gb|AAH63254.1| ☒ RIKEN cDNA 0610008A10 [Mus musculus]  
 Length = 258

Score = 233 bits (594), Expect = 2e-60  
 Identities = 169/254 (66%), Positives = 193/254 (75%), Gaps = 20/254 (7%)

Query: 4 VFFGCAFIAGFPM--MYVFTIAEEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGCAFIAGFP +Y+FTIA +PLR+IFLIAGAF LVSL+SS+ WF+ RV +N+D

Sbjct: 5 VFFGCAFIAGFPAFALYLFETIATDPLRVIFLIAGAFFWLVSLLLSSMFVFLVRVITNNRD 64

Query: 60 GPTQKYLLIFGAW--SWIQEMF--AAYKLLK-MSEGLKSINPGE-TAPSMRLM-YVSGLG 112  
 Q YLLIFGA IQE+F AAYKLLK SEGLKSINP E APSMRL+ YVSGLG

Sbjct: 65 ESQVQNYLLIFGALLSVCIQELFRLAYYKLLKKASEGLKSINPEEDIAPSMRLLAYVSGLG 124

Query: 113 FGIMSGVFSM--TSLSDSLGPGTVGIHGDSPPQFFLYSA-GTLVVIILLHVFWGIVFFDGCEM 169  
 FGIMSGVFS TLS+SLGPGTVGIHGDSPPQFFL SA TLV+I+LHVFWG+VFFDGCE

Sbjct: 125 FGIMSGVFSFVNTLSNSLGPVGIHGDSPPQFFLNSAFMTLVVIMLHVFWGVVFFDGCEK 184

Query: 170 -KW-GILLIALTHLLVSAQTFISSYYGINLM-AFIILVV-GTWAFIAAGGSCRS--XXXX 223  
 KW +L + LTHL+VS QTF+S YY +NL+ A+II+V+ G WAF AGGSCRS

Sbjct: 185 NKWYITLLTVLLTHLVVSTQTFLLSPYYEVNLVTAYIIMVLMGIWAFYVAGGSCRSCLKFCLL 244

Query: 224 XXXXXXXXYNQRSR 237  
 YNQRSR

Sbjct: 245 CQDKDFLLYNQRSR 258

☐ >gi|26324468|dbj|BAC25988.1| ☒ unnamed protein product [Mus musculus]  
 Length = 212

Score = 186 bits (471), Expect = 5e-46  
 Identities = 117/155 (75%), Positives = 127/155 (81%), Gaps = 12/155 (7%)

Query: 4 VFFGCAFIAGFPM--YVFTIAEEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGCAFIAGFP + YVFTIA +PLR+IFLIAGAF LVSL+SS+ WF+ RV DN+D

Sbjct: 5 VFFGCAFIAGFPALALYVFTIATDPLRVIFLIAGAFFWLVSLLLSSVFWFLVRVITDNRD 64

Query: 60 GPTQKYLLIFGAW--SWIQEMF--AAYKLLK-MSEGLKSINPGETAPSMRLM-YVSGLGF 113  
 GP Q YLLIFG IQE+F AAYKLLK SEGLKSINP ETAPSMRL+ YVSGLGF

Sbjct: 65 GPVQNYLLIFGVLLSVCIQELFRLAYYKLLKKASEGLKSINPEETAPSMRLLAYVSGLGF 124

Query: 114 GIMSGVFSM--TLSDSLGPGTVGIHGDSPQFFLYS 146  
 GIMSGVFS TLS+SLGPGTVGIHGDSPQFFL S  
 Sbjct: 125 GIMSGVFSFVNTLSNSLGPVTGVIHGDSPQFFLNS 159

☐ >gi|37077149|sp|Q8BVF7|AP1A MOUSE ☒ Gamma-secretase subunit APH-1A  
 gi|18848275|gb|AAH24111.1| ☒ 6530402N02Rik protein [Mus musculus]  
 Length = 265

Score = 176 bits (447), Expect = 2e-43  
 Identities = 124/234 (52%), Positives = 159/234 (67%), Gaps = 18/234 (7%)

Query: 4 VFFGCAFIAGFPM--MYVFTIAEEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGC F+AFGP +++ T+A +PLR+I L+AGAF LVSL++S+ WF+ D D  
 Sbjct: 5 VFFGCTFVAFGPAFSLFLITVAGDPLRVIIIVAGAFFWLVSLLLASVWVWVILVHVTDTRSD 64

Query: 60 GPTQKYLLIFGAWS--WIQEMF--AAYKLLKMS-EGLKSINPGETAP-SMRLM-YVSGLG 112  
 Q LLIFGA +QE+F AAYKLLK + EGL S++ +P S+R M YVSGL  
 Sbjct: 65 ARLQYGLLIFGAASVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLS 124

Query: 113 FGIMSGVFSMT--LSDSLGPGTVGIHGDSPQFFLYSAG-TLVIILLHVFHWGIVFFDGCCEM 169  
 FGI+SGVFS+ L+D+LGPG VGIHGDSP +FL SA T IILLH FWG+VFFD CE  
 Sbjct: 125 FGIISGVFSVINILADALGPGVVGIVHGDSPYYFLTSAFLTAAILLHTFWGVVFFDACER 184

Query: 170 K--WGILLIALTHLLVSAQTFISSYYGINLMAFIILVV--GTWAFIAAGGSCRS 219  
 + W + L+ +HLL S TF++ +Y +L+ + V G WAFI AGGS RS  
 Sbjct: 185 RRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRS 238

☐ >gi|12654775|gb|AAH01230.1| ☒ APH-1A protein [Homo sapiens]  
 Length = 265

Score = 176 bits (447), Expect = 3e-43  
 Identities = 124/234 (52%), Positives = 159/234 (67%), Gaps = 18/234 (7%)

Query: 4 VFFGCAFIAGFPM--MYVFTIAEEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGC F+AFGP +++ T+A +PLR+I L+AGAF LVSL++S+ WF+ D D  
 Sbjct: 5 VFFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVWVWVILVHVTDTRSD 64

Query: 60 GPTQKYLLIFGAWS--WIQEMF--AAYKLLKMS-EGLKSINPGETAP-SMRLM-YVSGLG 112  
 Q LLIFGA +QE+F AAYKLLK + EGL S++ +P S+R M YVSGL  
 Sbjct: 65 ARLQYGLLIFGAASVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLS 124

Query: 113 FGIMSGVFSMT--LSDSLGPGTVGIHGDSPQFFLYSAG-TLVIILLHVFHWGIVFFDGCCEM 169  
 FGI+SGVFS+ L+D+LGPG VGIHGDSP +FL SA T IILLH FWG+VFFD CE  
 Sbjct: 125 FGIISGVFSVINILADALGPGVVGIVHGDSPYYFLTSAFLTAAILLHTFWGVVFFDACER 184

Query: 170 K--WGILLIALTHLLVSAQTFISSYYGINLMAFIILVV--GTWAFIAAGGSCRS 219  
 + W + L+ +HLL S TF++ +Y +L+ + V G WAFI AGGS RS  
 Sbjct: 185 RRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSIRS 238

☐ >gi|37077707|sp|Q96BI3|AP1A HUMAN Gamma-secretase subunit APH-1A (APH-1a) (Aph-1  
 stabilization factor) (CGI-78) (UNQ579/PRO1141)  
 gi|15990414|gb|AAH15568.1| ☒ APH-1A protein [Homo sapiens]



gi|18088501|gb|AAH20590.1| **L** APH-1A protein [Homo sapiens]  
gi|25989510|gb|AAM61956.1| presenilin stabilization factor b [Homo sapiens]  
 Length = 265

Score = 176 bits (447), Expect = 3e-43  
 Identities = 124/234 (52%), Positives = 159/234 (67%), Gaps = 18/234 (7%)

Query: 4 VFFGCAFIAGFPM--MYVFTIAEEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGC F+AFGP +++ T+A +PLR+I L+AGAF LVSL++S+ WF+ D D  
 Sbjct: 5 VFFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVVWFILVHVTDRSD 64

Query: 60 GPTQKYLLIFGAWS--WIQEMF--AAYKLLKMS-EGLKSINPGETAP-SMRLM-YVSGLG 112  
 Q LLIFGA +QE+F AAYKLLK + EGL S++ +P S+R M YVSGL  
 Sbjct: 65 ARLQYGLLIFGAASVLLQEVFRFAYYKLLKKADEGLASLSEDGRSPISIRQMAYVSGLS 124

Query: 113 FGIMSGVFSMT--LSDSLGPGTVGIHGDSPQFFLYSAG-TLVIILLHVFHWGIVFFDGCCEM 169  
 FGI+SGVFS+ L+D+LGPG VGIHGDSP +FL SA T IILLH FWG+VFFD CE  
 Sbjct: 125 FGIISGVFSVINILADALGPGVVGIVHGDSPYYFLTSAFLTAAILLHTFWGVVFFDACER 184

Query: 170 K--WGILLIALTHLLVSAQTFISSYYGINLMAFIILVV--GTWAFIAAGGSCRS 219  
 + W + L+ +HLL S TF++ +Y +L+ + V G WAFI AGGS RS  
 Sbjct: 185 RRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRS 238

>gi|34858248|ref|XP\_345252.1| **L** similar to Aphla-pending protein [Rattus norvegi]  
 Length = 265

Score = 176 bits (446), Expect = 3e-43  
 Identities = 123/234 (52%), Positives = 159/234 (67%), Gaps = 18/234 (7%)

Query: 4 VFFGCAFIAGFPM--MYVFTIAEEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGC F+AFGP +++ T+A +PLR+I L+AGAF LVSL++S+ WF+ D D  
 Sbjct: 5 VFFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVVWFILVHVTDRSD 64

Query: 60 GPTQKYLLIFGAWS--WIQEMF--AAYKLLKMS-EGLKSINPGETAP-SMRLM-YVSGLG 112  
 Q LLIFGA +QE+F AAYKLLK + EGL S++ +P S+R M YVSGL  
 Sbjct: 65 ARLQYGLLIFGAASVLLQEVFRFAYYKLLKKADEGLASLSEDGRSPISIRQMAYVSGLS 124

Query: 113 FGIMSGVFSMT--LSDSLGPGTVGIHGDSPQFFLYSAG-TLVIILLHVFHWGIVFFDGCCEM 169  
 FGI+SGVFS+ L+D+LGPG VGIHGDSP +FL SA T IILLH FWG+VFFD CE  
 Sbjct: 125 FGIISGVFSVINILADALGPGVVGIVHGDSPYYFLTSAFLTAAILLHTFWGVVFFDACER 184

Query: 170 K--WGILLIALTHLLVSAQTFISSYYGINLMAFIILVV--GTWAFIAAGGSCRS 219  
 + W + L+ +HLL S TF++ +Y +L+ + V G WAF+ AGGS RS  
 Sbjct: 185 RRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFVITAGGSLRS 238

>gi|7705787|ref|NP\_057106.1| **L** CGI-78 protein [Homo sapiens]  
gi|4929623|gb|AAD34072.1| **L** CGI-78 protein [Homo sapiens]  
gi|24637562|gb|AAN63816.1| **L** presenilin stabilization factor [Homo sapiens]  
 Length = 251

Score = 173 bits (438), Expect = 3e-42  
 Identities = 124/234 (52%), Positives = 159/234 (67%), Gaps = 18/234 (7%)

Query: 4 VFFGCAFIAGFPM--MYVFTIAEEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59

VFFGC F+AFGP +++ T+A +PLR+I L+AGAF LVSL++S+ WF+ D D  
 Sbjct: 5 VFFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVWVWVILVHVTDRSD 64

Query: 60 GPTQKYLLIFGAWS--WIQEMF--AYYKLLKMS-EGLKSINPGETAP-SMRLM-YVSGLG 112  
 Q LLIFGA +QE+F AYYKLLK + EGL S++ +P S+R M YVSGL  
 Sbjct: 65 ARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEDGRSPISIRQMAYVSGLS 124

Query: 113 FGIMSGVFSMT--LSDSLGPGTVGIHGDSPQFFLYSAG-TLVIILLHVFWGIVFFDGCCEM 169  
 FGI+SGVFS+ L+D+LGPG VGIHGDSP +FL SA T IILLH FWG+VFFD CE  
 Sbjct: 125 FGIISGVFSVINILADALGPGVVGIVHGDSPYYFLTSAFLTAAILLHTFWGVVFFDACER 184

Query: 170 K--WGILLIALTHLLVSAQTFISSYYGINLMAFIILVV--GTWAFIAAGGSCRS 219  
 + W + L+ +HLL S TF++ +Y +L+ + V G WAFI AGGS RS  
 Sbjct: 185 RRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRS 238

☐ >gi|22203751|ref|NP\_666216.1| ☒ L anterior pharynx defective 1A homolog; anterior  
 1A homolog (C. elegans) [Mus musculus]  
 gi|15341753|gb|AAH12406.1| ☒ L Anterior pharynx defective 1A homolog [Mus musculus]  
 gi|34786036|gb|AAH57865.1| ☒ L Anterior pharynx defective 1A homolog [Mus musculus]  
 Length = 247

Score = 172 bits (436), Expect = 5e-42  
 Identities = 124/234 (52%), Positives = 159/234 (67%), Gaps = 18/234 (7%)

Query: 4 VFFGCAFIAGFPM--MYVFTIAEEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGC F+AFGP +++ T+A +PLR+I L+AGAF LVSL++S+ WF+ D D  
 Sbjct: 5 VFFGCTFVAFGPAFSLFLITVAGDPLRVIIIVAGAFFWLVSLLLASVWVWVILVHVTDRSD 64

Query: 60 GPTQKYLLIFGAWS--WIQEMF--AYYKLLKMS-EGLKSINPGETAP-SMRLM-YVSGLG 112  
 Q LLIFGA +QE+F AYYKLLK + EGL S++ +P S+R M YVSGL  
 Sbjct: 65 ARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEDGRSPISIRQMAYVSGLS 124

Query: 113 FGIMSGVFSMT--LSDSLGPGTVGIHGDSPQFFLYSAG-TLVIILLHVFWGIVFFDGCCEM 169  
 FGI+SGVFS+ L+D+LGPG VGIHGDSP +FL SA T IILLH FWG+VFFD CE  
 Sbjct: 125 FGIISGVFSVINILADALGPGVVGIVHGDSPYYFLTSAFLTAAILLHTFWGVVFFDACER 184

Query: 170 K--WGILLIALTHLLVSAQTFISSYYGINLMAFIILVV--GTWAFIAAGGSCRS 219  
 + W + L+ +HLL S TF++ +Y +L+ + V G WAFI AGGS RS  
 Sbjct: 185 RRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRS 238

☐ >gi|14250557|gb|AAH08732.1| ☒ L APH-1A protein [Homo sapiens]  
 gi|14550502|gb|AAH09501.1| ☒ L APH-1A protein [Homo sapiens]  
 gi|17389295|gb|AAH17699.1| ☒ L APH-1A protein [Homo sapiens]  
 gi|22761292|dbj|BAC11529.1| ☒ L unnamed protein product [Homo sapiens]  
 gi|25989508|gb|AAM61955.1| ☒ L presenilin stabilization factor a [Homo sapiens]  
 gi|37183020|gb|AAQ89310.1| ☒ L GAAV579 [Homo sapiens]  
 Length = 247

Score = 172 bits (436), Expect = 6e-42  
 Identities = 124/234 (52%), Positives = 159/234 (67%), Gaps = 18/234 (7%)

Query: 4 VFFGCAFIAGFPM--MYVFTIAEEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGC F+AFGP +++ T+A +PLR+I L+AGAF LVSL++S+ WF+ D D

Sbjct: 5 VFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSLLLASVWVFILVHVTDRSD 64

Query: 60 GPTQKYLLIFGAWS--WIQEMF--AAYKLLKMS-EGLKSINPGETAP-SMRLM-YVSGLG 112  
 Q LLIFGA +QE+F AAYKLLK + EGL S++ +P S+R M YVSGL

Sbjct: 65 ARLQYGLLIFGAASVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLS 124

Query: 113 FGIMSGVFSMT--LSDSLGPGTVGIHGDSPOFFLYSAG-TLVIILLHVFWGIVFFDGCCEM 169  
 FGI+SGVFS+ L+D+LGPG VGIHGDS +FL SA T IILLH FWG+VFFD CE

Sbjct: 125 FGIISGVFSVINILADALGPGVVGIIHGDSPIYFLTSAFLTAIILLHTFWGVVFFDACER 184

Query: 170 K--WGILLIALTHLLVSAQTFISSYYGINLMAFIILVV--GTWAFIAAGGSCRS 219  
 + W + L+ +HLL S TF++ +Y +L+ + V G WAFI AGGS RS

Sbjct: 185 RRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRS 238

☐ >gi|41056229|ref|NP\_956409.1| ☒ anterior pharynx defective 1B [Danio rerio]  
 gi|37077309|sp|Q8JHE9|AP1B\_BRARE Gamma-secretase subunit Aph-1b (Anterior-pharynx  
 1b)

gi|22001127|gb|AAM88325.1| ☒ Aph-1 protein [Danio rerio]  
 gi|37682171|gb|AAQ98012.1| ☒ anterior pharynx defective 1B-like [Danio rerio]  
 gi|47939453|gb|AAH71492.1| ☒ Unknown (protein for MGC:86848) [Danio rerio]  
 Length = 258

Score = 171 bits (433), Expect = 1e-41  
 Identities = 125/235 (53%), Positives = 164/235 (69%), Gaps = 20/235 (8%)

Query: 4 VFFGCAFIAGFPM--MYVFTIAEEPLRIIFLIAGAF--NLVSLLISSLWFMARVTIDNKD 59  
 VFFGC FIAFGP +++FTIA +PLR+IFLIAGAF + LL S +WF+ V I NK+

Sbjct: 5 VFFGCTFIAFGPAIALEFMTIARDPLRVIFLIAGAFFWLVSLLLSSLVWFIT-VQISNKN 63

Query: 60 GPTQKY-LLIFGA--WSWIQEMF--AAYKLLKMS-EGLKSINPGETAP-SMR-LMYVSGL 111  
 TQ+ LLIFG +QE F YY+LLK + EGL +++ +T P SMR L YVSGL

Sbjct: 64 SATQQRGLLIFGVVLSVLLQEAFFRYGYRLLKKANEGLLALSQEDTMPISMRQLAYVSGL 123

Query: 112 GFGIMSGVFSMT--LSDSLGPGTVGIHGDSPOFFLYSA-GTLVIILLHVFWGIVFFDGCCE 168  
 GFG MSG FS+ LSDSLGPGTVGIHG+S +F+ SA TL IILLH+FWG+VFF+ CE

Sbjct: 124 GFGFMGSAFVSVNLSLSDSLGPGTVGIHGESQHYFISSAFMTLAIILLHMFVGWVFFFEACE 183

Query: 169 MK--WGILLIALTHLLVSAQTFISSYYGINLM-AFIIL-VVGTWAFIAAGGSCRS 219  
 + W + + +HL+VS TF++ +Y +L+ +IIL V+ WA++ AGGS R+

Sbjct: 184 RQRWWALGAVVASHLVVSLTFVNPYQGS LIPTYIILSVMAVWAYLCAGGSLRN 238

☐ >gi|34864287|ref|XP\_343418.1| ☒ similar to RIKEN cDNA 0610008A10 [Rattus norvegi  
 Length = 216

Score = 171 bits (432), Expect = 1e-41  
 Identities = 135/249 (54%), Positives = 156/249 (62%), Gaps = 52/249 (20%)

Query: 4 VFFGCAFIAGFPM--YVFTIAEEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGCAFIAGFP + YVFTIA +PLR+IFLIAGAF LVSL+SS+ WF+ RV DN+D

Sbjct: 5 VFFGCAFIAGFPALSLYVFTIATDPLRVIFLIAGAFFWLVSLLLSSVFWFLVRVITDNRD 64

Query: 60 GPTQKYLLIFGAW--SWIQEMF--AAYKLLKMS-EGLKSINPGETAPSMRLMYVSGLGFG 114  
 GP Q YLLIFG IQE+F AYY+LLK + EGLKSINP ETAPSMRL+

Sbjct: 65 GPVQNYLLIFGVLLSVCIQELFRLAYYRLLKKANEGLKSINPEETAPSMRL----- 116

Query: 115 IMSGVFSMTLSDSLGPSTVGIHGDSPQFFLYSAGTLVIIILLHVFWGIVFFDGCCEM-KWGI 173  
 Y+ TLVII+LHVFWGIVFFDGCCE KW I  
 Sbjct: 117 -----AYAFMTLVIIMLHVFWGIVFFDGCCEKNKWI 147

Query: 174 -LLIALTHLLVSAQTFISSYYGINLM-AFIILVV-GTWAFIAAGGSCRS--XXXXXXXXXX 228  
 L + LTHLLVS QT +S +Y +NL+ A+II+V+ G WAF AGGS RS  
 Sbjct: 148 LLTVLLTHLLVSTQTLSPHYEVNLVTAYIIMVLMGIWAFVAGGSRRSLKLCLLCQDKD 207

Query: 229 XXXYNQRSR 237  
 YNQRSR  
 Sbjct: 208 FLLYNQRSR 216

☐ >gi|26347159|dbj|BAC37228.1| ☒ unnamed protein product [Mus musculus]  
 Length = 152

Score = 120 bits (301), Expect = 2e-26  
 Identities = 77/143 (53%), Positives = 97/143 (67%), Gaps = 9/143 (6%)

Query: 86 KMSEGLKSINPGETAP-SMRLM-YVSGLGFGIMSGVFSMT--LSDSLGPSTVGIHGDSPQ 141  
 K EGL S++ +P S+R M YVSGL FGI+SGVFS+ L+D+LGPG VGIHGDSP  
 Sbjct: 1 KADEGLASLSEDGRSPISIRQMAYVSGLSFGIISGVFSVINILADALGPGVVGIHGDSPY 60

Query: 142 FFLYSAG-TLVIILLHVFWGIVFFDGCCEMK--WGILLIALTHLLVSAQTFISSYYGINLM 198  
 +FL SA T IILLH FWG+VFFD CE + W + L+ +HLL S TF++ +Y +L+  
 Sbjct: 61 YFLTSAFLTAAIILLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLL 120

Query: 199 AFIILVV--GTWAFIAAGGSCRS 219  
 + V G WAFI AGGS RS  
 Sbjct: 121 PIYAVTVSMGLWAFITAGGSLRS 143

☐ >gi|31233667|ref|XP\_318923.1| ENSANGP00000015809 [Anopheles gambiae]  
 gi|30174614|gb|EAA14158.2| ENSANGP00000015809 [Anopheles gambiae str. PEST]  
 Length = 247

Score = 117 bits (294), Expect = 2e-25  
 Identities = 97/237 (40%), Positives = 140/237 (59%), Gaps = 22/237 (9%)

Query: 1 MTMV-FFGCAFIAGFP--MMYVFTIAEEPLRIIFLIAGAFN-LVSLLISSLWFMARVTID 56  
 MT+V FFGC+F+AFGP M+ TIA +P+RII LIA +F LVSL+SS ++A +  
 Sbjct: 7 MTVVEFFGCSFLAFGPPVAMFALTIAHDPIRIILIAASFFWLVSLLSSTVWLAHPVT 66

Query: 57 NKDGPTQKYLLIFGAWSWIQEMFAY--YKLLKMSE-GLKSINPGETAPSMR--LMYVSGL 111  
 +K + LI + + + F Y YK+L+ +E GL+ + R L Y SGL  
 Sbjct: 67 SK----VTFLGICSVFIQVCKRFRYLMYKVLKTESGLQEVTDIVRIADYRHILSYASGL 122

Query: 112 GFGIMSGVFSMT--LSDSLGPSTVGIHGDSPQFFLYSAG-TLVIILLHVFWGIVFFDGCCE 168  
 GFGI+SG FS+ L+DS+GP TVG+ S F L SA +L +ILLH FW ++FF+ C+  
 Sbjct: 123 GFGIISGAFSLVNILADSVGPATVGLKAASDIFMLISAAQSLAMILLHTFWSVIFFNACD 182

Query: 169 MK--WGILLIALTHLLVSAQTFI--SSYYGINLMA--FIILVVGWAFIAAGGSCRS 219  
 +K + I + +HL VS T + S Y + L+ ++ + G AF AGG+ S  
 Sbjct: 183 VKNYHYHIGYVVASHLFVSCMTLLNASGLYAVTLLISYTMVCITGAIAFQVAGGTVAS 239